IRS construct used to make transgenic plants: NPTII gene shown in gray; *ΔRBCS1B::LUC* fusion consisted of *RBCS1B* sequences spanning from the PflMI site in *RBCS1B* exon I to the BsmI site in exon III; Firefly Luciferase nos 3' terminator is cloned in frame to the truncated *RBCS1B* exon III. *RBCS2B RBCS3B* sequences normally downstream of *RBCS1B* were placed 3' to the *ΔRBCS1B::LUC* fusion. Figure 1C shows a positive control construct (pJGJ204) consisting of a *RBCS1B* promoter *RBCS1B::LUC* gene fusion. Half arrows represent the approximate location and direction of oligonucleotide primers (o13 and o14) used in PCR reactions. Restriction enzymes: **P**, PflMI; **B**, BsmI; and **S**, SphI.

B1

IN THE CLAIMS:

Please replace claim 1 with the following clean copy of the amended claim. A marked up copy showing the amendment is provided in Appendix A.

1. (amended) A method of identifying homologous recombination in plant cells, the method comprising:

contacting a plurality of plant cells with a heterologous nucleic acid molecule encoding a fusion protein comprising a polypeptide sequence of interest linked to a reporter sequence, wherein the nucleic acid molecule lacks sequences necessary for expression of the fusion protein in a cell; and

detecting the presence of the reporter activity in the plant cells, thereby identifying plant cells in which homologous recombination has occurred between the introduced heterologous nucleic acid molecule and endogenous plant DNA.

B2 SUB E1

REMARKS

Claims 1-12 are currently under examination, claims 13-31 are withdrawn from consideration by the Examiner. A copy of all of the claims under examination are provided in Appendix B, attached hereto.

The amendments add no new matter and are fully supported throughout the application.